

SEQUENCE LISTING

<110> YOKOYAMA, KEIICHI  
NAKAMURA, NAMI  
MIWA, TETSUYA  
SEGURO, KATSUYA

<120> PROCESS FOR PRODUCING MICROBIAL TRANSGLUTAMINASE

<130> 0010-0937-0

<140> 09/109,063  
<141> 1998-07-02

<150> JP 180010/1997  
<151> 1997-07-04

<160> 62

<170> PatentIn Ver. 2.0

<210> 1  
<211> 331  
<212> PRT  
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<400> 1  
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20 25 30  
Asn Tyr Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg  
35 40 45  
Lys Gln Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys  
50 55 60  
Val Gly Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu  
65 70 75 80  
Ala Phe Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn  
85 90 95  
Gly Arg Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val  
100 105 110  
Ala Lys Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu  
115 120 125

Val Ala Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser  
 130 135 140  
 Ala Tyr Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala  
 145 150 155 160  
 Leu Arg Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn  
 165 170 175  
 Thr Pro Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg  
 180 185 190  
 Met Lys Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg  
 195 200 205  
 Ser Ser Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg  
 210 215 220  
 Pro Ala Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile  
 225 230 235 240  
 Pro Arg Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr  
 245 250 255  
 Gly Trp Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp  
 260 265 270  
 Thr His Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met  
 275 280 285  
 His Val Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp  
 290 295 300  
 Phe Asp Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn  
 305 310 315 320  
 Thr Ala Pro Asp Lys Val Lys Gln Gly Trp Pro  
 325 330

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 Asp Ser Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met

48

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cca gat cca tat cgt cca tct tat ggt cgt gct gaa act gtt gtt aat Pro Asp Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn				96
20	25	30		
aat tat att cgt aaa tgg caa caa gtt tat tct cat cgt gat ggt cgt Asn Tyr Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg				144
35	40	45		
aaa caa caa atg act gaa gaa caa cgt gaa tgg ctg tct tat ggt tgc Lys Gln Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys				192
50	55	60		
gtt ggt gtt act tgg gtt aac tct ggt cag tat ccg act aac cgt ctg Val Gly Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu				240
65	70	75	80	
gca ttc gct tcc ttc gat gaa gat cgt ttc aag aac gaa ctg aag aac Ala Phe Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn				288
85	90	95		
ggt cgt ccg cgt tct ggt gaa act cgt gct gaa ttc gaa ggt cgt gtt Gly Arg Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val				336
100	105	110		
gct aag gaa tcc ttc gat gaa gag aaa ggc ttc cag cgt gct cgt gaa Ala Lys Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu				384
115	120	125		
gtt gct tct gtt atg aac cgt gct cta gag aac gct cat gat gaa tct Val Ala Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser				432
130	135	140		
gct tac ctg gat aac ctg aag aag gaa ctg gct aac ggt aac gat gct Ala Tyr Leu Asp Asn Leu Lys Glu Leu Ala Asn Gly Asn Asp Ala				480
145	150	155	160	
ctg cgt aac gaa gat gct cgt tct ccg ttc tac tct gct ctg cgt aac Leu Arg Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn				528
165	170	175		
act ccg tcc ttc aaa gaa cgt aac ggt ggt aac cat gat ccg tct cgt Thr Pro Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg				576
180	185	190		
atg aaa gct gtt atc tac tct aaa cat ttc tgg tct ggt cag gat aga Met Lys Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg				624
195	200	205		
tct tct tct gct gat aaa cgt aaa tac ggt gat ccg gat gca ttc cgt Ser Ser Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg				672
210	215	220		
ccg gct ccg ggt act ggt ctg gta gac atg tct cgt gat cgt aac atc Pro Ala Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile				720

225	230	235	240	
ccg cgt tct ccg act tct ccg ggt gaa ggc ttc gtt aac ttc gat tac Pro Arg Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr 245 250 255				768
ggt tgg ttc ggt gct cag act gaa gct gat gct gat aag act gta tgg Gly Trp Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp 260 265 270				816
acc cat ggt aac cat tac cat gct ccg aac ggt tct ctg ggt gct atg Thr His Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met 275 280 285				864
cat gta tac gaa tct aaa ttc cgt aac tgg tct gaa ggt tac tct gac His Val Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp 290 295 300				912
ttc gat cgt ggt gct tac gtt atc acc ttc att ccg aaa tct tgg aac Phe Asp Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn 305 310 315 320				960
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cca gct gaa cca ctg gat cgt atg cca gat cca tat cgt cca tct tat Pro Ala Glu Pro Leu Asp Arg Met Pro Asp Pro Tyr Arg Pro Ser Tyr 10 15 20 25				161
ggt cgt gct gaa act gtt gtt aat aat tat att cgt aaa tgg caa caa Gly Arg Ala Glu Thr Val Val Asn Asn Tyr Ile Arg Lys Trp Gln Gln 30 35 40				209
gtt tat tct cat cgt gat ggt cgt aaa caa caa atg act gaa gaa caa Val Tyr Ser His Arg Asp Gly Arg Lys Gln Gln Met Thr Glu Glu Gln				257

45

50

55

cgt gaa tgg ctg tct tat ggt tgc gtt ggt act tgg gtt aac tct			305
Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly Val Thr Trp Val Asn Ser			
60	65	70	
ggt cag tat ccg act aac cgt ctg gca ttc gct tcc ttc gat gaa gat			353
Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe Ala Ser Phe Asp Glu Asp			
75	80	85	
cgt ttc aag aac gaa ctg aag aac ggt cgt ccg cgt tct ggt gaa act			401
Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg Pro Arg Ser Gly Glu Thr			
90	95	100	105
cgt gct gaa ttc gaa ggt cgt gtt gct aag gaa tcc ttc gat gaa gag			449
Arg Ala Glu Phe Glu Gly Arg Val Ala Lys Glu Ser Phe Asp Glu Glu			
110	115	120	
aaa ggc ttc cag cgt gct cgt gaa gtt gct tct gtt atg aac cgt gct			497
Lys Gly Phe Gln Arg Ala Arg Glu Val Ala Ser Val Met Asn Arg Ala			
120	125	130	135
cta gag aac gct cat gat gaa tct gct tac ctg gat aac ctg aag aag			545
Leu Glu Asn Ala His Asp Glu Ser Ala Tyr Leu Asp Asn Leu Lys Lys			
140	145	150	
gaa ctg gct aac ggt aac gat gct ctg cgt aac gaa gat gct cgt tct			593
Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg Asn Glu Asp Ala Arg Ser			
155	160	165	
ccg ttc tac tct gct ctg cgt aac act ccg tcc ttc aaa gaa cgt aac			641
Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro Ser Phe Lys Glu Arg Asn			
170	175	180	185
ggt ggt aac cat gat ccg tct cgt atg aaa gct gtt atc tac tct aaa			689
Gly Gly Asn His Asp Pro Ser Arg Met Lys Ala Val Ile Tyr Ser Lys			
190	195	200	
cat ttc tgg tct ggt cag gat aga tct tct tct gct gat aaa cgt aaa			737
His Phe Trp Ser Gly Gln Asp Arg Ser Ser Ala Asp Lys Arg Lys			
205	210	215	
tac ggt gat ccg gat gca ttc cgt ccg gct ccg ggt act ggt ctg gta			785
Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala Pro Gly Thr Gly Leu Val			
220	225	230	
gac atg tct cgt gat cgt aac atc ccg cgt tct ccg act tct ccg ggt			833
Asp Met Ser Arg Asp Arg Asn Ile Pro Arg Ser Pro Thr Ser Pro Gly			
235	240	245	
gaa ggc ttc gtt aac ttc gat tac ggt tgg ttc ggt gct cag act gaa			881
Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp Phe Gly Ala Gln Thr Glu			
250	255	260	265
gct gat gct gat aag act gta tgg acc cat ggt aac cat tac cat gct			929
Ala Asp Ala Asp Lys Thr Val Trp Thr His Gly Asn His Tyr His Ala			

270	275	280	
ccg aac ggt tct ctg ggt gct atg cat gta tac gaa tct aaa ttc cgt Pro Asn Gly Ser Leu Gly Ala Met His Val Tyr Glu Ser Lys Phe Arg			977
285	290	295	
aac tgg tct gaa ggt tac tct gac ttc gat cgt ggt gct tac gtt atc Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp Arg Gly Ala Tyr Val Ile			1025
300	305	310	
acc ttc att ccg aaa tct tgg aac act gct ccg gac aaa gtt aaa cag Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala Pro Asp Lys Val Lys Gln			1073
315	320	325	
ggg tgg ccg taatgaaaagc ttggatctct aattactgga cttcacacag Gly Trp Pro			1122
330			
actaa <u>gg</u> atag acatatctta tattatgtga ttttgtgaca tttccttagat gtgaggtgga			1182
<u>gg</u> tgatgtat aaggtagatg atgatcctct acgccggacg catcggtggcc ggcacacccg			1242
gcgcacagg tgccgttgct ggccctata tcgcccacat caccgatggg gaagatcggg			1302
ctcg <u>cc</u> actt cgggctcatg agcgcttggat tcggcgtggg tatggggca gcggccgtgg			1362
ccggggact gttgggcgcc atctccttgc atgcaccatt cttgcggcg gcggtgctca			1422
acgg <u>cc</u> caa cctactactg ggctgcttcc taatgcagga gtcgcataag ggagagcg			1482
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aattcatcgat ttagtaagga ggttaaaaat ggattctga			39
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<211> 41			
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<223> Description of Artificial Sequence:SYNTHETIC DNA			
<400> 5			
cgatcgtag aatccatttt aaacccctt actaatcgat g			41

<210> 6  
<211> 41  
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<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:SYNTHETIC DNA

<400> 6  
cgatcgtgtt actccaccag ctgaaccact ggatcgtatg c 41

<210> 7  
<211> 41  
<212> DNA  
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<223> Description of Artificial Sequence:SYNTHETIC DNA

<400> 7  
gatctggcat acgatccagt ggttcagctg gtggagtaac a 41

<210> 8  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:SYNTHETIC DNA

<400> 8  
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<210> 9  
<211> 41  
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<400> 9  
attaacaaca gtttcagcac gaccataaga tggacgatat g 41

<210> 10  
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<223> Description of Artificial Sequence:SYNTHETIC DNA

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<400> 15  
agcttgttaa cccaaagtaac accaacgcaa ccataagaca 40

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<400> 16  
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<400> 17  
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<210> 18  
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<400> 18  
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<223> Description of Artificial Sequence:SYNTHETIC DNA

<400> 22  
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<210> 24  
<211> 42  
<212> DNA  
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<223> Description of Artificial Sequence:SYNTHETIC DNA

<400> 24

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<210> 25  
<211> 39  
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<223> Description of Artificial Sequence:SYNTHETIC DNA

<400> 25  
agctttctag agcacggttc ataacagaag caacttcac 39

<210> 26  
<211> 45  
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<223> Description of Artificial Sequence:SYNTHETIC DNA

<400> 26  
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<210> 27  
<211> 50  
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<220>  
<223> Description of Artificial Sequence:SYNTHETIC DNA

<400> 27  
cttcttcagg ttatccaggt aagcagattc atcatgagcg ttctcttagag 50

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<220>  
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<400> 28  
ctgaagaagg aactggctaa cggttaacgat gctctgcgta acgaagatg 49

<210> 29  
<211> 49  
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<400> 29  
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<210> 30  
<211> 40  
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<223> Description of Artificial Sequence:SYNTHETIC DNA

<400> 30  
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<210> 31  
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<400> 31  
cttgaaaggc cgaggatgttta cgcaagcagc agtagaaacg 39

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<210> 34

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<210> 36  
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<400> 36  
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<210> 37  
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<223> Description of Artificial Sequence:SYNTHETIC DNA

<400> 37  
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<210> 38  
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<400> 43  
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<210> 45  
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<400> 45  
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<223> Description of Artificial Sequence:SYNTHETIC DNA

<400> 53

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38

<210> 54

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:SYNTHETIC DNA

<400> 54

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38

<210> 55

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:SYNTHETIC DNA

<400> 55

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34

<210> 56

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:SYNTHETIC DNA

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20

<210> 57

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<212> DNA

<213> Artificial Sequence

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<400> 57  
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<210> 58  
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<400> 58  
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<210> 59  
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<220>  
<223> Description of Artificial Sequence:SYNTHETIC DNA

<400> 59  
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<210> 60  
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<220>  
<223> Description of Artificial Sequence:N-TERMINAL FRAGMENT

<400> 60  
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1 5

<210> 61  
<211> 15  
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<220>  
<223> Description of Artificial Sequence:CODON FOR N-TERMINAL FRAGMENT

<400> 61  
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<210> 62  
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<220>  
<223> Description of Artificial Sequence:N-TERMINAL  
FRAGMENT

<400> 62  
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